SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Xu, Wenfeng
Presnell, Scott R.
Yee, David P.
Foster, Donald C.

(ii) TITLE OF THE INVENTION: PROTEASE-ACTIVATED RECEPTOR
PAR4 (ZCHEMR2)

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: ZymoGenetics, Inc.
  (B) STREET: 1201 Eastlake Avenue East
  (C) CITY: Seattle
  (D) STATE: WA
  (E) COUNTRY: USA
  (F) ZIP: 98102

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Leith, Debra K
  (B) REGISTRATION NUMBER: 32,619
  (C) REFERENCE/DOCKET NUMBER: 98-10

(ix) TELECOMMUNICATION INFORMATION:
    (A) TELEPHONE: 206-442-6674
    (B) TELEFAX: 206-442-6678
    (C) TELEX:

    (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 4895 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ix) FEATURE:

    (A) NAME/KEY: Coding Sequence
    (B) LOCATION: 176...1330
    (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CTCCCACGGG CTGGCTGGCA AGCGGCCCTG GTGGGTCTGC GGGGGCAGGG GCAGCCTTCC      60
TGGTTTATCT CCACCGGCGC GATCTGCTCG TCCGCCTCGG CTCCAGAAGC TGGGGCTCAG     120
GGTCCGGCGA GGCAGGAAGC CTGAGGCCAC AGCCCAGAGC AGCCTGAGTG CAGTC ATG      178
                                                            Met
                                                            1
```

```
TGG GGG CGA CTG CTC CTG TGG CCC CTG GTG CTG GGG TTC AGC CTG TCT      226
Trp Gly Arg Leu Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu Ser
              5                   10                  15
```

```
GGC GGC ACC CAG ACC CCC AGC GTC TAC GAC GAG AGC GGG AGC ACC GGA      274
Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr Gly
          20                  25                  30
```

```
GGT GGT GAT GAC AGC ACG CCC TCA ATC CTG CCT GCC CCC CGC GGC TAC      322
Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly Tyr
      35                  40                  45
```

```
CCA GGC CAA GTC TGT GCC AAT GAC AGT GAC ACC CTG GAG CTC CCG GAC      370
Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro Asp
50                  55                  60                  65
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```
AGC TCA CGG GCA CTG CTT CTG GGC TGG GTG CCC ACC AGG CTG GTG CCC        418
Ser Ser Arg Ala Leu Leu Leu Gly Trp Val Pro Thr Arg Leu Val Pro
                70                  75                  80

GCC CTC TAT GGG CTG GTC CTG GTG GTG GGG CTG CCG GCC AAT GGG CTG        466
Ala Leu Tyr Gly Leu Val Leu Val Val Gly Leu Pro Ala Asn Gly Leu
                85                  90                  95

GCG CTG TGG GTG CTG GCC ACG CAG GCA CCT CGG CTG CCC TCC ACC ATG        514
Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr Met
            100                 105                 110

CTG CTG ATG AAC CTC GCG ACT GCT GAC CTC CTG CTG GCC CTG GCG CTG        562
Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu Ala Leu
            115                 120                 125

CCC CCG CGG ATC GCC TAC CAC CTG CGT GGC CAG CGC TGG CCC TTC GGG        610
Pro Pro Arg Ile Ala Tyr His Leu Arg Gly Gln Arg Trp Pro Phe Gly
130                 135                 140                 145

GAG GCC GCC TGC CGC CTG GCC ACG GCC GCA CTC TAT GGT CAC ATG TAT        658
Glu Ala Ala Cys Arg Leu Ala Thr Ala Ala Leu Tyr Gly His Met Tyr
            150                 155                 160

GGC TCA GTG CTG CTG CTG GCC GCC GTC AGC CTG GAT CGC TAC CTG GCC        706
Gly Ser Val Leu Leu Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala
            165                 170                 175

CTG GTG CAC CCG CTG CGG GCC CGC GCC CTG CGT GGC CGG CGC CTG GCC        754
Leu Val His Pro Leu Arg Ala Arg Ala Leu Arg Gly Arg Arg Leu Ala
            180                 185                 190

CTT GGA CTC TGC ATG GCT GCT TGG CTC ATG GCG GCC GCC CTG GCA CTG        802
Leu Gly Leu Cys Met Ala Ala Trp Leu Met Ala Ala Ala Leu Ala Leu
            195                 200                 205

CCC CTG ACA CTG CAG CGG CAG ACC TTC CGG CTG GCG CGC TCC GAT CGC        850
Pro Leu Thr Leu Gln Arg Gln Thr Phe Arg Leu Ala Arg Ser Asp Arg
210                 215                 220                 225

GTG CTC TGC CAT GAC GCG CTG CCC CTG GAC GCA CAG GCC TCC CAC TGG        898
Val Leu Cys His Asp Ala Leu Pro Leu Asp Ala Gln Ala Ser His Trp
            230                 235                 240
```

```
CAA CCG GCC TTC ACC TGC CTG GCG CTG TTG GGC TGT TTC CTG CCC CTG        946
Gln Pro Ala Phe Thr Cys Leu Ala Leu Leu Gly Cys Phe Leu Pro Leu
            245             250             255

CTG GCC ATG CTG CTG TGC TAC GGG GCC ACC CTG CAC ACG CTG GCG GCC        994
Leu Ala Met Leu Leu Cys Tyr Gly Ala Thr Leu His Thr Leu Ala Ala
            260             265             270

AGC GGC CGG CGC TAC GGC CAC GCG CTG AGG CTG ACC GCA GTG GTG CTG        1042
Ser Gly Arg Arg Tyr Gly His Ala Leu Arg Leu Thr Ala Val Val Leu
            275             280             285

GCC TCC GCC GTG GCC TTC TTC GTG CCC AGC AAC CTG CTG CTG CTG CTG        1090
Ala Ser Ala Val Ala Phe Phe Val Pro Ser Asn Leu Leu Leu Leu Leu
290             295             300             305

CAT TAC TCG GAC CCG AGC CCC AGC GCC TGG GGC AAC CTC TAT GGT GCC        1138
His Tyr Ser Asp Pro Ser Pro Ser Ala Trp Gly Asn Leu Tyr Gly Ala
            310             315             320

TAC GTG CCC AGC CTG GCG CTG AGC ACC CTC AAC AGC TGC GTG GAT CCC        1186
Tyr Val Pro Ser Leu Ala Leu Ser Thr Leu Asn Ser Cys Val Asp Pro
            325             330             335

TTC ATC TAC TAC TAC GTG TCG GCC GAG TTC AGG GAC AAG GTG CGG GCA        1234
Phe Ile Tyr Tyr Tyr Val Ser Ala Glu Phe Arg Asp Lys Val Arg Ala
            340             345             350

GGG CTC TTC CAA CGG TCG CCG GGG GAC ACC GTG GCC TCC AAG GCC TCT        1282
Gly Leu Phe Gln Arg Ser Pro Gly Asp Thr Val Ala Ser Lys Ala Ser
            355             360             365

GCG GAA GGG GGC AGC CGG GGC ATG GGC ACC CAC TCC TCT TTG CTC CAG T      1331
Ala Glu Gly Gly Ser Arg Gly Met Gly Thr His Ser Ser Leu Leu Gln
370             375             380             385

GACACAAAGT GGGGAAGGCT GTACTGGGTC GAACAGGGTC CCTTCCCCCA CTTCACGTCC       1391
TTCCTGGGAC CTCAGAATGT GACCTTATTT GGAAATAGGG TTGTTACAAC TGTCACTAGC       1451
GGAGGTCACT TTGGAGAAGG GTGGGCCTTA CATCCAGTGT GGGTGGTGTC CTCATAAGAT       1511
AAGGAGAGGC CAGGCCTGGT GGCTCACGCC TGTAATCCCA GCACTTTAAG AGGCCAAGGC       1571
GGATGGATCA CTTGAGCCCA GGAGTTCAAC ACCAGCCTGA GCAACATGGT AAAACCCCAT       1631
CTCTACCAAA AATACAAAAA TTAGCTGGGC TTGGTGGCTG GCGCCTGTAA TCCCAGCTAC       1691
TCAGGAGACT GAGGCAGAAG GATCGCTTGA ACCTGGGAGG CAGAGGTTGC AGTGAGCCGA       1751
GATTGCGCCA CTGGACTCCA GCCTGCGTGA CAGAGAGCCT GTCTCTAAAT TAATTAATTA       1811
ATTAATTTAA TTCAATTTTA AAAAGACGAA AAGTGACGGC CAGGTGCAGT GGCTCACGCC       1871
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TATAATCTCA GCACTCTGGG AGGCCAAGAT GGAGGATTGC TTGAAGCCAG GAGTTTGGGA 1931
CCAGCCTGGG CAACATAGGG GGATCCCATC TCTACACACA AAAAAATTTT TTAATGAACC 1991
AGGCATTGTG GCATGCGCCT ATAGTCCCAG CCACTCAAGA GGCACAGGCG GGAGGATCAC 2051
TTGAGCCTGG GAGGTTGTGG TTGCAGTGAG CTATGATTGT ACCACTGCAC TCCAGCCTGG 2111
GCAACAGAGC AAGACCTTGT CTCAAAAATA AACAAACTAA AATTAAAAAA AGAAGACGAG 2171
AGATAGTGGG TGTGGTGGCT CACACCTGCA ATCCCAGCAC TTTGGAAGGC CGAGGTGGGC 2231
AGATCATCTG AGGCCAGGAG TTCAAGACCA GCCTGGCTAA CATGGTGAAA TCCTATCTCT 2291
ACCAAAAATA CAAAAATTAG CCAGGCGTGG TGGTGGGCAC CTGTACTGGG GAGGTGCCCA 2351
CCCAGCTACT GGGGAGGCTG AGTCAGGAGA ATCGCTTGAA CCTGGGAGGC GGAGGTTGCG 2411
GTCAGCTGAG ATGGTGCCAC TGCACTCCAG CCTGGGCGAA AGAGCGACTC TGTCTCCAAA 2471
AAAAAGAGAA GAGGAGAGGA CACAGAGACA CACAGAGAAG AAAGCCATGT GGCGGCAGAG 2531
GCAGAGATGG GAGTGATGCG GACGGACACA AACTAAGGGA TGCCACGATG CCAAGCACAG 2591
CCAACAGCCA CCAGCAGCCA GGAGACAGGC CTGGGACGGG CTCTCCCTCA CAGCCTCCAG 2651
AGGGAACCAG CCCTGCCACC ACCTTGACCC TGGACTTCTG GCCTGCAGAA CTGTGAGACA 2711
ATAAACTCTC ATTGTTTTAA GCTGCCTGGC ATGTGGCACT TTGTCAGGGC AGCCCAGGAA 2771
TCTGAAACAG GATCAAACTC TGCTTCCTGG GCCCTGCCAG CATCTCTGGC TCGGCTTTCT 2831
GGGCTGGATG CAGCCCACGA CGCACTGGTG TCTGAGATGG GGCTGGAGCT GGGGCTGGGG 2891
CTGCATTCCC TGGAGACTCA CTGCAAGTTC CTGCCCAGGA GGCTGAGGGC ACCCCATCCT 2951
CAGTGCCCAA TGCTGTGGCC CCACCAGGCC CAGAGCCTGG TTGGCCATTC TCATGCCCAC 3011
CAGCTTCTGG CTTTGGGATG TCTCTTGAGC AACCAGAATA GCACCCCCAA CTCTGCTCCC 3071
CAAAACCCAT CACTAGCACG GCTCAGCCTC CTGCTATCCC CTGACTGCTG GGGACCCTCG 3131
CCTTCCCTCC TCTCACCTGC AGGCTGATCC TTCTTTTCAC TTTCTGTCAA TGTCACCAGG 3191
GATAAGGTGG GACAATGGGG GGTGGGGGTG GACAGTGTGT GCTGGGGGGT TCGGGTGCTG 3251
CAGACCTGGA ACTCCCTTCT GCCAGGATGT TGGCAGCCGG TTGTAAGCCT TGCACGGGAC 3311
AGACCACACC CACCGCAACC TCATCCCCTC AGCACTAACC ACATCCACTC TCAACCCCGT 3371
CCCCTTCGCA CTGACCACAC CCACCCCGTT CGGCCCCGCC CCCCGCACTG AACACTCCCG 3431
CCCTCAACCC CGCACCCTCC GCACTCACCT CCCCCTCGCC GCTCGACCCC GCCCTCACCA 3491
CACTGACCAC CCTCAACCCA TTGCGCCCAG TCCCCACCAC AGTGACCACA CCCTCACTGG 3551
CTCGGCCCTG CCCCCAGTAT ACTGACCATT CCCCAGCCAC TTCCCTTCCG CACTTACCAC 3611
TCCCCCAGCC ACGCCCCTCC CCGCTGACCG CTCCTCCAGC CCCGCCTCCC CCGTACAGGC 3671
AGAGCGCCCG CCCACCTCTA TGCTGCGTTC TCCTGACTTT ACGTTGGCCC CTCCTCTGCC 3731
AAGCCCCCAG GGGAGCCCTC CCTGGCGTCC GAGGGTGGGA GTCGGGGTGT GGCAGGCCGC 3791
GGTGGGGGGC GGCAGTGGCT CCGCGCACTC ACCCGGGCCC CGGGCAGGGG CGCGCTCCAC 3851
TTCGTTGCAC GCGGGTCCGG CGCACAGTTC CCGGGCGAGT GGGCTGTGCG TGCTGACGTT 3911
GTAGAAGCGA GTGGCCTCGA AGGCTACGGG ACGAGGGTGG CGGGTGACCA AGTGCAGGCG 3971
CGACGGGTCA GGGACCGGGC CGGGCCGGGG GTGCGGGCGC GCGGGCCTAC CGGGTTCGTA 4031
GTAGTCGTAC ACGGAGACTG GCAGCGCCGA CGTCCTGCCC ACCACGCACT CCCGGAGAGC 4091
ACGGAACCGC ACGCACGTCA GGCACCGGCT GGGGATCTGT GGGGCAGCGG CGGGCGCAGG 4151
CTCGACCCGG GCCAGGAGGC CCGGGGCGCT GAGCTCAGGC CCAGAACTGG CTGATTTCAG 4211
GGATACCCAG GACGCGTGAA ACACAGAAGA AACGTGATCC CATTTTCTTT TTTTCTTTTA 4271
CTTTTCTTTT TTTTTTTTTT TCCTGAGACA GAGTCTCGCG CTGTTGCCCA GGCTGGAGTG 4331
CAGTGGCGTG ATCTCGGCTC ACTGCAAGCT CGGCCTCCTG GGTTCAAATG ATTCTCCTGC 4391
CTCAGCCTCC CAAGTAGCTG GGATAACAGG CGCCCACCAC CGCACCCTGC TAATTTTTTG 4451
TATTTTTGAT CAAGACGGAG TTTCACCATG TTGGCCAGGC TGGTCTCCAA CTCCTGCCCT 4511
CAAGTGATCC GCCTCGGTCC CATTTTTTAT TCTTTGGGTC CTTCCATCCC ACTGGGAAAA 4571
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CGTCTCAGGT GGCCTCTGAA ACACCACTCC TTTTTGTGTG TGTGCACGCA TGGCTGAGCA   4631
TGTGTGGGTG GGAGTCAGCA CATTCACGAT ACTGTGCAAT CATCACCTCT GTCTAGTTAC   4691
AGGACGGTTT CTTTCTCCCC CAAAGAAACC CCATCGCCAT CAGCACTCAC TCCCCACTCC   4751
CCCAGCCCCT GGCAACCACA AATCTTTCCA ACTCTACGGA TTTGCCTGTT CTGGGCATTT   4811
CATGTCAATG GAATCATGTA CTCTGTGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA   4871
AAAAAAAAAA AAAAAAAAAA AAAA                                          4895
```

        (2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 385 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein
        (v) FRAGMENT TYPE: internal

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Trp Gly Arg Leu Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu
1               5               10              15
Ser Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr
                20              25              30
Gly Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly
            35              40              45
Tyr Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro
    50              55              60
Asp Ser Ser Arg Ala Leu Leu Leu Gly Trp Val Pro Thr Arg Leu Val
65              70              75              80
Pro Ala Leu Tyr Gly Leu Val Leu Val Val Gly Leu Pro Ala Asn Gly
            85              90              95
Leu Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr
            100             105             110
Met Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu Ala
        115             120             125
Leu Pro Pro Arg Ile Ala Tyr His Leu Arg Gly Gln Arg Trp Pro Phe
    130             135             140
Gly Glu Ala Ala Cys Arg Leu Ala Thr Ala Ala Leu Tyr Gly His Met
145             150             155             160
Tyr Gly Ser Val Leu Leu Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu
                165             170             175
Ala Leu Val His Pro Leu Arg Ala Arg Ala Leu Arg Gly Arg Arg Leu
            180             185             190
```

```
Ala Leu Gly Leu Cys Met Ala Ala Trp Leu Met Ala Ala Ala Leu Ala
        195             200             205
Leu Pro Leu Thr Leu Gln Arg Gln Thr Phe Arg Leu Ala Arg Ser Asp
    210             215             220
Arg Val Leu Cys His Asp Ala Leu Pro Leu Asp Ala Gln Ala Ser His
225             230             235             240
Trp Gln Pro Ala Phe Thr Cys Leu Ala Leu Leu Gly Cys Phe Leu Pro
            245             250             255
Leu Leu Ala Met Leu Leu Cys Tyr Gly Ala Thr Leu His Thr Leu Ala
            260             265             270
Ala Ser Gly Arg Arg Tyr Gly His Ala Leu Arg Leu Thr Ala Val Val
        275             280             285
Leu Ala Ser Ala Val Ala Phe Phe Val Pro Ser Asn Leu Leu Leu Leu
    290             295             300
Leu His Tyr Ser Asp Pro Ser Pro Ser Ala Trp Gly Asn Leu Tyr Gly
305             310             315             320
Ala Tyr Val Pro Ser Leu Ala Leu Ser Thr Leu Asn Ser Cys Val Asp
            325             330             335
Pro Phe Ile Tyr Tyr Tyr Val Ser Ala Glu Phe Arg Asp Lys Val Arg
            340             345             350
Ala Gly Leu Phe Gln Arg Ser Pro Gly Asp Thr Val Ala Ser Lys Ala
        355             360             365
Ser Ala Glu Gly Gly Ser Arg Gly Met Gly Thr His Ser Ser Leu Leu
    370             375             380
Gln
385
```

                    (2) INFORMATION FOR SEQ ID NO:3:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1155 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
ATGTGGGGNM GNYTNYTNYT NTGGCCNYTN GTNYTNGGNT TYWSNYTNWS NGGNGGNACN    60
CARACNCCNW SNGTNTAYGA YGARWSNGGN WSNACNGGNG GNGGNGAYGA YWSNACNCCN   120
WSNATHYTNC CNGCNCCNMG NGGNTAYCCN GGNCARGTNT GYGCNAAYGA YWSNGAYACN   180
YTNGARYTNC CNGAYWSNWS NMGNGCNYTN YTNYTNGGNT GGGTNCCNAC NMGNYTNGTN   240
CCNGCNYTNT AYGGNYTNGT NYTNGTNGTN GGNYTNCCNG CNAAYGGNYT NGCNYTNTGG   300
GTNYTNGCNA CNCARGCNCC NMGNYTNCCN WSNACNATGY TNYTNATGAA YYTNGCNACN   360
GCNGAYYTNY TNYTNGCNYT NGCNYTNCCN CCNMGNATHG CNTAYCAYYT NMGNGGNCAR   420
```

```
MGNTGGCCNT TYGGNGARGC NGCNTGYMGN YTNGCNACNG CNGCNYTNTA YGGNCAYATG    480
TAYGGNWSNG TNYTNYTNYT NGCNGCNGTN WSNYTNGAYM GNTAYYTNGC NYTNGTNCAY    540
CCNYTNMGNG CNMGNGCNYT NMGNGGNMGN MGNYTNGCNY TNGGNYTNTG YATGGCNGCN    600
TGGYTNATGG CNGCNGCNYT NGCNYTNCCN YTNACNYTNC ARMGNCARAC NTTYMGNYTN    660
GCNMGNWSNG AYMGNGTNYT NTGYCAYGAY GCNYTNCCNY TNGAYGCNCA RGCNWSNCAY    720
TGGCARCCNG CNTTYACNTG YYTNGCNYTN YTNGGNTGYT TYYTNCCNYT NYTNGCNATG    780
YTNYTNTGYT AYGGNGCNAC NYTNCAYACN YTNGCNGCNW SNGGNMGNMG NTAYGGNCAY    840
GCNYTNMGNY TNACNGCNGT NGTNYTNGCN WSNGCNGTNG CNTTYTTYGT NCCNWSNAAY    900
YTNYTNYTNY TNYTNCAYTA YWSNGAYCCN WSNCCNWSNG CNTGGGGNAA YYTNTAYGGN    960
GCNTAYGTNC CNWSNYTNGC NYTNWSNACN YTNAAYWSNT GYGTNGAYCC NTTYATHTAY   1020
TAYTAYGTNW SNGCNGARTT YMGNGAYAAR GTNMGNGCNG GNYTNTTYCA RMGNWSNCCN   1080
GGNGAYACNG TNGCNWSNAA RGCNWSNGCN GARGGNGGNW SNMGNGGNAT GGGNACNCAY   1140
WSNWSNYTNY TNCAR                                                    1155
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 7 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Ile Thr Thr Cys His Asp Val
1               5
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 42 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
1               5                   10                  15
Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr
                20                  25                  30
```

```
Lys Asp Asp Asp Asp Lys Leu Glu Gly Gly
        35                  40
```

       (2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 8 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Asp Tyr Lys Asp Asp Asp Asp Lys
 1               5
```

       (2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 6 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Gly Tyr Pro Gly Gln Val
 1               5
```

       (2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 6 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Phe Leu Leu Arg Asn
1   5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 22 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGGCACTGCC CCTGACACTG CA   22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCGTAGCAC AGCAGCATGG   20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 18 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTGCCCGCC CTCTATGG   18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCGCGAGGTT CATCAGCA   18